

## Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>SERIAL NUMBER:</u> <u>10/518,072</u>
<b>ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE</b>		
1 <input type="checkbox"/> Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <input type="checkbox"/> Invalid Line Length	The rules require that a line <b>not exceed</b> 72 characters in length. This includes white spaces.	
3 <input type="checkbox"/> Misaligned Amino Numbering	The numbering under each 5 <sup>th</sup> amino acid is misaligned. Do <b>not</b> use tab codes between numbers; use space characters, instead.	
4 <input type="checkbox"/> Non-ASCII	The submitted file was <b>not saved</b> in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <input type="checkbox"/> Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. <b>Per Sequence Rules, each n or Xaa can only represent a single residue.</b> Please present the <b>maximum</b> number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <input type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. <b>This applies to the mandatory &lt;220&gt;-&lt;223&gt; sections for Artificial or Unknown sequences.</b>	
7 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) <b>This sequence is intentionally skipped</b>  Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 <input type="checkbox"/> Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 <input type="checkbox"/> Use of <220>	Sequence(s) <u>128</u> missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 <input type="checkbox"/> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <input type="checkbox"/> Misuse of n/Xaa	"n" can only represent a single <u>nucleotide</u> ; "Xaa" can only represent a single <u>amino acid</u>	



IFWP

**RAW SEQUENCE LISTING**  
**PATENT APPLICATION: US/10/518,072**

**DATE: 12/20/2005**  
**TIME: 10:31:35**

**Input Set : A:\263365US0XPCT.txt**  
**Output Set: N:\CRF4\12202005\J518072.raw**

```

3 <110> APPLICANT: Weill, Mylene
4     Fort, Philippe
5     Raymond, Michel
6     Pasteur, Nicole
8 <120> TITLE OF INVENTION: NOVEL ACETYLCHOLINESTERASE GENE RESPONSIBLE FOR
9     INSECTICIDE RESISTANCE AND APPLICATIONS THEREOF
11 <130> FILE REFERENCE: 263365US0XPCT
13 <140> CURRENT APPLICATION NUMBER: 10/518,072
14 <141> CURRENT FILING DATE: 2004-12-16
16 <150> PRIOR APPLICATION NUMBER: FR 02/07622
17 <151> PRIOR FILING DATE: 2002-06-20
19 <150> PRIOR APPLICATION NUMBER: FR 02/13799
20 <151> PRIOR FILING DATE: 2002-11-05
23 <160> NUMBER OF SEQ ID NOS: 129
25 <170> SOFTWARE: PatentIn version 2.1
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 524
29 <212> TYPE: PRT
30 <213> ORGANISM: Anopheles gambiae
32 <400> SEQUENCE: 1
33 Asp Pro Leu Val Val Asn Thr Asp Lys Gly Arg Ile Arg Gly Ile Thr
34      1           5           10          15
36 Val Asp Ala Pro Ser Gly Lys Lys Val Asp Val Trp Leu Gly Ile Pro
37      20          25          30
39 Tyr Ala Gln Pro Pro Val Gly Pro Leu Arg Phe Arg His Pro Arg Pro
40      35          40          45
42 Ala Glu Lys Trp Thr Gly Val Leu Asn Thr Thr Pro Pro Asn Ser
43      50          55          60
45 Cys Val Gln Ile Val Asp Thr Val Phe Gly Asp Phe Pro Gly Ala Thr
46      65          70          75          80
49 Met Trp Asn Pro Asn Thr Pro Leu Ser Glu Asp Cys Leu Tyr Ile Asn
50      85          90          95
52 Val Val Ala Pro Arg Pro Arg Pro Lys Asn Ala Ala Val Met Leu Trp
53      100         105         110
55 Ile Phe Gly Gly Phe Tyr Ser Gly Thr Ala Thr Leu Asp Val Tyr
56      115         120         125
58 Asp His Arg Ala Leu Ala Ser Glu Glu Asn Val Ile Val Val Ser Leu
59      130         135         140
61 Gln Tyr Arg Val Ala Ser Leu Gly Phe Leu Phe Leu Gly Thr Pro Glu
62      145         150         155         160
64 Ala Pro Gly Asn Ala Gly Leu Phe Asp Gln Asn Leu Ala Leu Arg Trp
65      165         170         175
67 Val Arg Asp Asn Ile His Arg Phe Gly Gly Asp Pro Ser Arg Val Thr

```

Does Not Comply  
corrected Diskette Neede  
*pp 6-7*

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**Input Set : A:\263365US0XPCT.txt**  
**Output Set: N:\CRF4\12202005\J518072.raw**

68	180	185	190
70	Leu Phe Gly Glu Ser Ala Gly Ala Val Ser Val Ser Leu His Leu Leu		
71	195	200	205
73	Ser Ala Leu Ser Arg Asp Leu Phe Gln Arg Ala Ile Leu Gln Ser Gly		
74	210	215	220
76	Ser Pro Thr Ala Pro Trp Ala Leu Val Ser Arg Glu Glu Ala Thr Leu		
77	225	230	235
79	240	245	250
80	Arg Ala Leu Arg Leu Ala Glu Ala Val Gly Cys Pro His Glu Pro Ser		255
82	83	260	265
85	Lys Leu Ser Asp Ala Val Glu Cys Leu Arg Gly Lys Asp Pro His Val		270
86	275	280	285
88	Leu Val Asn Asn Glu Trp Gly Thr Leu Gly Ile Cys Glu Phe Pro Phe		
89	290	295	300
91	Leu Ala Ser Gly Arg Phe Lys Lys Thr Glu Ile Leu Thr Gly Ser Asn		
92	305	310	315
94	320	325	330
95	335	340	345
97	Arg Lys Glu Glu Gly Val Thr Val Thr Arg Glu Glu Phe Leu Gln Ala		350
98	350	355	360
100	Val Arg Glu Leu Asn Pro Tyr Val Asn Gly Ala Ala Arg Gln Ala Ile		365
101	365	370	375
103	Val Phe Glu Tyr Thr Asp Trp Thr Glu Pro Asp Asn Pro Asn Ser Asn		
104	380	390	395
106	400	405	410
107	415	420	425
109	430	435	440
110	445	450	455
112	460	465	470
113	475	480	485
115	490	495	500
116	505	510	515
118	520		
119			
121			
122			
124			
125			
127			
128			
130			
131			
135	<210> SEQ ID NO: 2		
136	<211> LENGTH: 1932		
137	<212> TYPE: DNA		
138	<213> ORGANISM: Anopheles gambiae		
140	<220> FEATURE:		
141	<221> NAME/KEY: CDS		

**RAW SEQUENCE LISTING**  
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**DATE: 12/20/2005**  
**TIME: 10:31:35**

**Input Set : A:\263365US0XPCT.txt**  
**Output Set: N:\CRF4\12202005\J518072.raw**

142 <222> LOCATION: (1)..(1932)  
144 <400> SEQUENCE: 2  
145 atg ttt gtg tgt tgt ttt ttc ttt ctc tct ctc tct ttc tgt ggt tcc 48  
146 Met Phe Val Cys Cys Phe Phe Leu Ser Leu Ser Phe Cys Gly Ser  
147 1 5 10 15  
149 aac att tca gac gca ttt ttt aca cca tat ata ggt cac ggt gag tcc 96  
150 Asn Ile Ser Asp Ala Phe Phe Thr Pro Tyr Ile Gly His Gly Glu Ser  
151 20 25 30  
153 gta cga att ata gat gcc gag ttg ggc acg ctc gag cat gtc cac agt 144  
154 Val Arg Ile Ile Asp Ala Glu Leu Gly Thr Leu Glu His Val His Ser  
155 35 40 45  
157 gga gca acg ccg cgg cga cgc ctg acg agg cgc gag tca aac tcg 192  
158 Gly Ala Thr Pro Arg Arg Gly Leu Thr Arg Arg Glu Ser Asn Ser  
159 50 55 60  
161 gac gcg aac gac aac gat ccg ctg gtg gtc aac acg gat aag ggg cgc 240  
162 Asp Ala Asn Asp Asn Asp Pro Leu Val Val Asn Thr Asp Lys Gly Arg  
163 65 70 75 80  
165 atc cgc ggc att acg gtc gat gcg ccc agc ggc aag aag gtg gac gtg 288  
166 Ile Arg Gly Ile Thr Val Asp Ala Pro Ser Gly Lys Lys Val Asp Val  
167 85 90 95  
169 tgg ctc ggc att ccc tac gcc cag ccg gtc ggg cgc cta cgg ttc 336  
170 Trp Leu Gly Ile Pro Tyr Ala Gln Pro Pro Val Gly Pro Leu Arg Phe  
171 100 105 110  
173 cgt cat ccg cgg ccg gcc gaa aag tgg acc ggc gtg ctg aac acg acc 384  
174 Arg His Pro Arg Pro Ala Glu Lys Trp Thr Gly Val Leu Asn Thr Thr  
175 115 120 125  
177 aca ccg ccc aac agc tgc gtg cag atc gtg gac acc gtg ttc ggc gac 432  
178 Thr Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr Val Phe Gly Asp  
179 130 135 140  
181 ttc ccg ggc gcg acc atg tgg aac ccg aac acg ccc ctg tcc gag gac 480  
182 Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro Leu Ser Glu Asp  
183 145 150 155 160  
185 tgt ctg tac att aac gtg gtg gca ccg cga ccc cgg ccc aag aat gcg 528  
186 Cys Leu Tyr Ile Asn Val Val Ala Pro Arg Pro Arg Pro Lys Asn Ala  
187 165 170 175  
189 gcc gtc atg ctg tgg atc ttc ggc ggc ttc tac tcc ggc acc gcc 576  
190 Ala Val Met Leu Trp Ile Phe Gly Gly Phe Tyr Ser Gly Thr Ala  
191 180 185 190  
193 acc ctg gac gtg tac gac cac ccg gcg ctt gcg tcg gag gag aac gtg 624  
194 Thr Leu Asp Val Tyr Asp His Arg Ala Leu Ala Ser Glu Glu Asn Val  
195 195 200 205  
197 atc gtg gtg tcg ctg cag tac cgc gtg gcc agt ctg ggc ttc ctg ttt 672  
198 Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly Phe Leu Phe  
199 210 215 220  
201 ctc ggc acc ccg gaa gcg ccg ggc aat gcg gga ctg ttc gat cag aac 720  
202 Leu Gly Thr Pro Glu Ala Pro Gly Asn Ala Gly Leu Phe Asp Gln Asn  
203 225 230 235 240  
205 ctt gcg cta cgc tgg gtg ccg gac aac att cac ccg ttc ggt ggc gat 768  
206 Leu Ala Leu Arg Trp Val Arg Asp Asn Ile His Arg Phe Gly Gly Asp

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**Output Set: N:\CRF4\12202005\J518072.raw**

207	245	250	255	
209	ccg tcg cgt gtg aca ctg ttc ggc gag agt gcc ggt gcc gtc tcg gtg			816
210	Pro Ser Arg Val Thr Leu Phe Gly Glu Ser Ala Gly Ala Val Ser Val			
211	260	265	270	
213	tcg ctg cat ctg ctg tcc gcc ctt tcc cgc gat ctg ttc cag cgg gcc			864
215	Ser Leu His Leu Leu Ser Ala Leu Ser Arg Asp Leu Phe Gln Arg Ala			
216	275	280	285	
218	atc ctg cag agc ggc tcg ccg acg gca ccg tgg gca ttg gta tcg cgc			912
219	Ile Leu Gln Ser Gly Ser Pro Thr Ala Pro Trp Ala Leu Val Ser Arg			
220	290	295	300	
222	gag gaa gcc aca cta aga gca ctg cgg ttg gcc gag gcg gtc ggc tgc			960
223	Glu Glu Ala Thr Leu Arg Ala Leu Arg Leu Ala Glu Ala Val Gly Cys			
224	305	310	315	320
226	ccg cac gaa ccg agc aag ctg agc gat gcg gtc gag tgc ctg cgc ggc			1008
227	Pro His Glu Pro Ser Lys Leu Ser Asp Ala Val Glu Cys Leu Arg Gly			
228	325	330	335	
230	aag gac ccg cac gtg ctg gtc aac aac gag tgg ggc acg ctc ggc att			1056
231	Lys Asp Pro His Val Leu Val Asn Asn Glu Trp Gly Thr Leu Gly Ile			
232	340	345	350	
234	tgc gag ttc ccg ttc gtg ccg gtg gtc gac ggt gcg ttc ctg gac gag			1104
235	Cys Glu Phe Pro Phe Val Pro Val Val Asp Gly Ala Phe Leu Asp Glu			
236	355	360	365	
238	acg ccg cag cgt tcg ctc gcc agc ggg cgc ttc aag aag acg gag atc			1152
239	Thr Pro Gln Arg Ser Leu Ala Ser Gly Arg Phe Lys Lys Thr Glu Ile			
240	370	375	380	
242	ctc acc ggc agc aac acg gag gag ggc tac tac ttc atc atc tac tac			1200
243	Leu Thr Gly Ser Asn Thr Glu Glu Gly Tyr Tyr Phe Ile Ile Tyr Tyr			
244	385	390	395	400
246	ctg acc gag ctg ctg cgc aag gag gag ggc gtg acc gtg acg cgc gag			1248
247	Leu Thr Glu Leu Leu Arg Lys Glu Glu Gly Val Thr Val Thr Arg Glu			
248	405	410	415	
250	gag ttc ctg cag ggc gtg cgc gag ctc aac ccg tac gtg aac ggg gcg			1296
251	Glu Phe Leu Gln Ala Val Arg Glu Leu Asn Pro Tyr Val Asn Gly Ala			
252	420	425	430	
254	gcc cgg cag gcg atc gtg ttc gag tac acc gac tgg acc gag cgc gac			1344
255	Ala Arg Gln Ala Ile Val Phe Glu Tyr Thr Asp Trp Thr Glu Pro Asp			
256	435	440	445	
258	aac ccg aac agc aac cgg gac ggc ctg gac aag atg gtg ggc gac tat			1392
259	Asn Pro Asn Ser Asn Arg Asp Ala Leu Asp Lys Met Val Gly Asp Tyr			
260	450	455	460	
262	cac ttc acc tgc aac gtg aac gag ttc ggc cag cgg tac gcc gag gag			1440
263	His Phe Thr Cys Asn Val Asn Glu Phe Ala Gln Arg Tyr Ala Glu Glu			
264	465	470	475	480
266	ggc aac aac gtc tac atg tat ctg tac acg cac cgc agc aaa ggc aac			1488
267	Gly Asn Asn Val Tyr Met Tyr Leu Tyr Thr His Arg Ser Lys Gly Asn			
268	485	490	495	
270	ccg tgg ccg cgc tgg acg ggc gtg atg cac ggc gac gag atc aac tac			1536
271	Pro Trp Pro Arg Trp Thr Gly Val Met His Gly Asp Glu Ile Asn Tyr			
272	500	505	510	

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/518,072

DATE: 12/20/2005  
TIME: 10:31:35

Input Set : A:\263365US0XPCT.txt  
Output Set: N:\CRF4\12202005\J518072.raw

274	gtg	tac	acc	gac	gag	1584												
275	Val	Phe	Gly	Glu	Pro	Leu	Asn	Pro	Thr	Leu	Gly	Tyr	Thr	Glu	Asp	Glu		
276	515				520								525					
278	aaa	gac	ttt	agc	cgg	aag	atc	atg	cga	tac	tgg	tcc	aac	ttt	gcc	aaa		
279	Lys	Asp	Phe	Ser	Arg	Lys	Ile	Met	Arg	Tyr	Trp	Ser	Asn	Phe	Ala	Lys		
280	530					535							540					
282	acc	ggg	aat	cca	aat	ccc	aac	acg	gcc	agc	agc	gaa	tac	ccc	gag	tgg		
283	Thr	Gly	Asn	Pro	Asn	Pro	Asn	Pro	Asn	Thr	Ala	Ser	Ser	Glu	Phe	Pro	Glu	Trp
284	545					550							555			560		
286	ccc	aag	cac	acc	gcc	cac	gga	cgg	cac	tat	ctg	gag	ctg	ggc	ctc	aac	1728	
287	Pro	Lys	His	Thr	Ala	His	Gly	Arg	His	Tyr	Leu	Glu	Leu	Gly	Leu	Asn		
288	565					565					570			575				
291	acg	tcc	tcc	gtc	gtt	cgg	ggc	cca	cgg	ttg	agg	cag	tgt	gcc	ttc	tgg	1776	
292	Thr	Ser	Phe	Val	Gly	Arg	Gly	Pro	Arg	Leu	Arg	Gln	Cys	Ala	Phe	Trp		
293	580					585							590					
295	aag	aag	tac	ctt	ccc	cag	cta	gtt	gca	gct	acc	tcg	aac	cta	cca	ggg	1824	
296	Lys	Lys	Tyr	Leu	Pro	Gln	Leu	Val	Ala	Ala	Thr	Ser	Asn	Leu	Pro	Gly		
297	595					600							605					
299	cca	gca	ccg	cct	agt	gaa	ccg	tgc	gaa	agc	agc	gca	ttt	ttt	tac	cga	1872	
300	Pro	Ala	Pro	Pro	Ser	Glu	Pro	Cys	Glu	Ser	Ser	Ala	Phe	Phe	Tyr	Arg		
301	610					615							620					
303	cct	gat	ctg	atc	gtg	ctg	ctg	gtg	tcg	ctg	ctt	acg	gcg	acc	gtc	aga		
304	Pro	Asp	Leu	Ile	Val	Leu	Leu	Val	Ser	Leu	Leu	Thr	Ala	Thr	Val	Arg		
305	625					630							635			640		
307	ttc	ata	caa	taa												1932		
308	Phe	Ile	Gln															
311	<210>	SEQ	ID	NO:	3													
312	<211>	LENGTH:	643															
313	<212>	TYPE:	PRT															
314	<213>	ORGANISM:	Anopheles gambiae															
316	<400>	SEQUENCE:	3															
317	Met	Phe	Val	Cys	Cys	Phe	Phe	Phe	Leu	Ser	Leu	Ser	Phe	Cys	Gly	Ser		
318	1				5				10					15				
320	Asn	Ile	Ser	Asp	Ala	Phe	Phe	Thr	Pro	Tyr	Ile	Gly	His	Gly	Glu	Ser		
321					20				25					30				
323	Val	Arg	Ile	Ile	Asp	Ala	Glu	Leu	Gly	Thr	Leu	Glu	His	Val	His	Ser		
324					35				40					45				
326	Gly	Ala	Thr	Pro	Arg	Arg	Arg	Gly	Leu	Thr	Arg	Arg	Glu	Ser	Asn	Ser		
327					50				55					60				
329	Asp	Ala	Asn	Asp	Asn	Asp	Pro	Leu	Val	Val	Asn	Thr	Asp	Lys	Gly	Arg		
330	65					70				75				80				
332	Ile	Arg	Gly	Ile	Thr	Val	Asp	Ala	Pro	Ser	Gly	Lys	Lys	Val	Asp	Val		
333						85				90				95				
335	Trp	Leu	Gly	Ile	Pro	Tyr	Ala	Gln	Pro	Pro	Val	Gly	Pro	Leu	Arg	Phe		
336						100				105				110				
338	Arg	His	Pro	Arg	Pro	Ala	Glu	Lys	Trp	Thr	Gly	Val	Leu	Asn	Thr	Thr		
339						115				120				125				
341	Thr	Pro	Pro	Asn	Ser	Cys	Val	Gln	Ile	Val	Asp	Thr	Val	Phe	Gly	Asp		
342						130				135				140				

10/578,072 6

<210> SEQ ID NO 128  
<211> LENGTH: 20  
<212> TYPE: DNA  
<213> ORGANISM: Artificial  
<220> FEATURE:  
<221> NAME/KEY: MISC\_FEATURE  
<222> LOCATION: (6)..(6)  
<223> OTHER INFORMATION: n=a,c,g, or t  
<400> SEQUENCE: 128  
ccgggngcsa cyatgtggaa

needs explanation - see item 11 on  
Euro summary  
sheet

RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/10/518,072

DATE: 12/20/2005  
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Input Set : A:\263365US0XPCT.txt  
Output Set: N:\CRF4\12202005\J518072.raw

9

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:128; N Pos. 6

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:39,40,41,42,43,44,45,46,47,48,49,50,54,55,58,59,123,124,128,129

**VERIFICATION SUMMARY**  
**PATENT APPLICATION: US/10/518,072**

**DATE: 12/20/2005**  
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L:6024 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:128 after pos.:0